

FIG. 1

Splice variant and domain organization of MTSP4

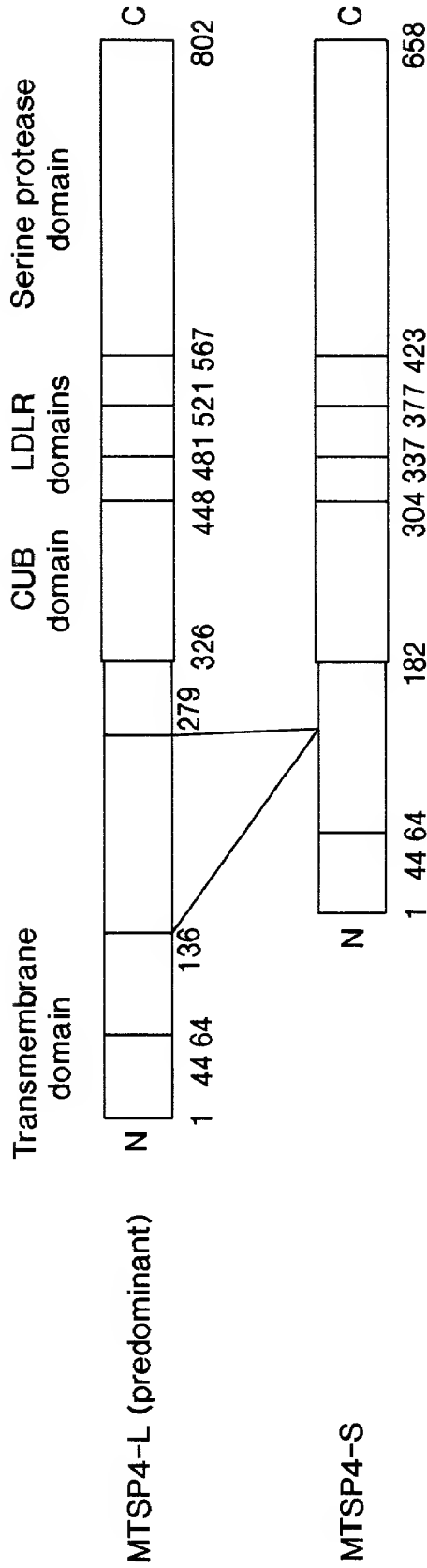


FIG. 2

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Madison *et al.*

Pat. No.:

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February 2, 2001

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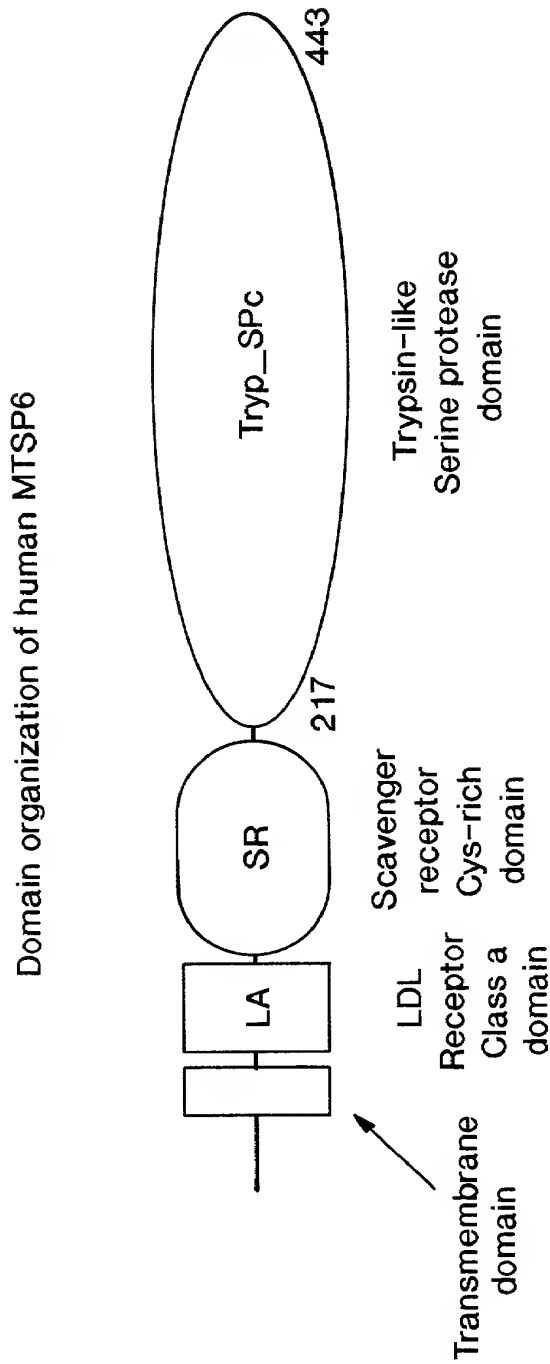


FIG. 3

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▽

MTSP3	194	LACGKS-----LKT	PRVVGEEASVDSWPQVSIQYDKQHVC	CGGSILD	236
				205	
MTSP4-S	396	PQCDGRPD	CRDGSDEEHCEGLQGPSSRIVG	GAVSSEGEWPQASLQVRGRHICGGALIA	455
				424	
MTSP4-L	540	PQCDGRPD	CRDGSDEEHCEGLQGPSSRIVG	GAVSSEGEWPQASLQVRGRHICGGALIA	599
				568	
MTSP6	205	TACGHR-----RGYSSRIVGGNMSLLSQWPQASLQFQGYHLCGGSVIT			248
				217 +	
MTSP3	237	PHWVLTA	AHCFRKHTDVFN--WKVRAGSDKLGS---	FPSLAVAKIIIEFNPMYPKDND	290
MTSP4-S	456	DRWVITA	AHCFQEDSMAS	TVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYD	515
MTSP4-L	600	DRWVITA	AHCFQEDSMAS	TVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYD	718
MTSP6	249	PLWIITA	AHCVYDLYLPKS--WTIQVGLVSLD--NPAPSHLVEKIVYH	SKYKPKRLGND	304
MTSP3	291	IALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWII	IGWGFTKQNGGKMSDILLQASVQV		350
				*	
MTSP4-S	516	VALLQLDHPVVRSA	AVRPVCLPARSHFFEPGLHCWITGWGALRE-GGPISNALQKVDVQL		574
				*	
MTSP4-L	660	VALLQLDHPVVRSA	AVRPVCLPARSHFFEPGLHCWITGWGALRE-GGPISNALQKVDVQL		718
				*	
MTSP6	305	IALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTS	SGWGATED-GGDASPVLNHA	AVPL	363
				*	
MTSP3	351	IDSTRCNADDAYQGEVTEKMMCAGI	PEGGVDTCCQDSSGGPLMYQSDQ--WHVVGIVSWGY		408
MTSP4-S	575	IPQDLCS--EVYRYQVTPRMLCAGYRKGKKDACQGDSSGGPLVCKALSGRWFLAGLVSWGL			632
MTSP4-L	719	IPQDLCS--EVYRYQVTPRMLCAGYRKGKKDACQGDSSGGPLVCKALSGRWFLAGLVSWGL			776
MTSP6	364	ISNKICNHRDVYGGII	SPSMLCAGYLTGGVDSCQGDSSGPLVCQERR-LWKVLVGATSFGI		442
MTSP3	409	GCGGPSTPGVYTKVSAYLNWIYNVWKAEL			437
MTSP4-S	633	GCGRPNYFGVYTRITGVISWIIQQVVT			658
MTSP4-L	777	GCGRPNYFGVYTRITGVISWIIQQVVT			802
MTSP6	423	GCAEVNKP	GVYTRVTSFLDWIHEQMERDLKT		453

▽ cleavage site

+ potential glycosylation site

* unpaired cysteine

FIG. 4